

$\beta 1\alpha 1$

*Nco*I      ▼  
-2 CCATGGGCAGAGACTCCCCAAGGGATTCTGTGTACCAAGGGCTGTGCTACTACACC 60  
M G R D S P R D F V Y Q F K G L C Y Y T  
61    AACGGGACGCAGCGCATACGGGATGTGATCAGATACTACAAACCAGGAGGAGTACCTG 120  
N G T Q R I R D V I R Y I Y N Q E E Y L  
121    CGCTACGACAGCGACGTGGCGAGTACCGCGCGCTGACCGAGCTGGGGCGGCCCTCAGCC 180  
R Y D S D V G E Y R A L T E L G R P S A  
181    GAGTACTTTAACAAAGCAGTACCTGGAGCAGACGCCGGCCGAGCTGGACACGGTCTGCAGA 240  
E Y F N K Q Y L E Q T R A E L D T V C R  
end of  $\beta 1$  ▼ start of  $\alpha 1$   
241    CACAAC TACGAGGGGT CGGAGGT CCGCACCTCCCTGC GGGCGCTTGGAGGTCAAGACGAC 300  
H N Y E G S E V R T S L R R L G G Q D D  
301    ATTGAGGCCGACCACGTAGCCGCCTATGGTATAAAATATGTATCAGTATTATGAATCCAGA 360  
I E A D H V A A Y G I N M Y Q Y Y E S R  
361    GGCCAGTTCACACATGAATTGATGGT GACGAGGAATTCTATGTGGACTTGGATAAGAAG 420  
G Q F T H E F D G D E E F Y V D L D K K  
421    GAGACCACATCTGGAGGATCCCCGAGTTGGACAGCTGACAAGCTTGACCCCCAAGGTGGA 480  
E T I W R I P E F G Q L T S F D P Q G G  
481    CTTCAAAATATAGCTATAATAAAACACAATTGGAAATCTGATGAAGAGGTCAAATTCA 540  
L Q N I A I I K H N L E . I L M K R S N S  
541    ACCCAAGCTGTCAACTAACTCGAG      *Xba*I  
T Q A V N end

FIG. 1A

FIG. 1B

$\beta 1\alpha 1/MBP-72-89$

NcoI  
CCATGGCCAGAGACTCCCCACAGAAGGCCAGGGACTCAGGATGAGAACCCAGTGGTGCACTTGGAGGGGGCTCACTAGTCCCCGAGGCTCT  
 M G R D S P Q K S Q R T Q D E N P V H F G G G S L V P R G S  
 GGAGGGTGGAGGCTCC  
 G G G G S  
 |---linker---|

FIG. 1C

$\beta 1\alpha 1/MBP-55-69$

NcoI  
CCATGGCCAGAGACTCCTCGGCAAGGATTCGCATCATGGGGGGACGACCCACTACGGTGGAGGGCTCACTAGTG  
 M G R D S S G K D S H H A A R T T H Y G G G G S L V

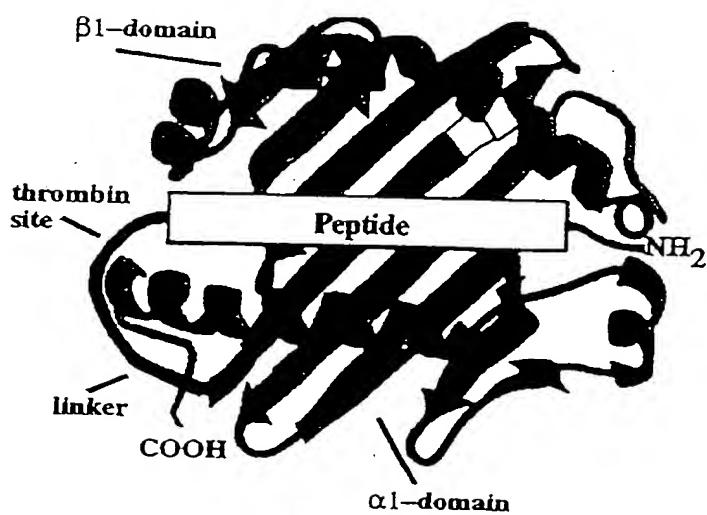
FIG. 1D

$\beta 1\alpha 1/CM-2$

NcoI  
CCATGGCCAGAGACTCCAAACTGGAACTGGCAGTCCGCTCTGGAAACCTGAACCTGAAACGGGCTCCCTGAAACGGGCTGGAGGGCTCACTAGTG  
 M G R D S K L E L Q S A L E A S L E H G G G G S L V



a. RT1.B



b.  $\beta 1\alpha 1/\text{peptide}$

FIG. 2  
3/15

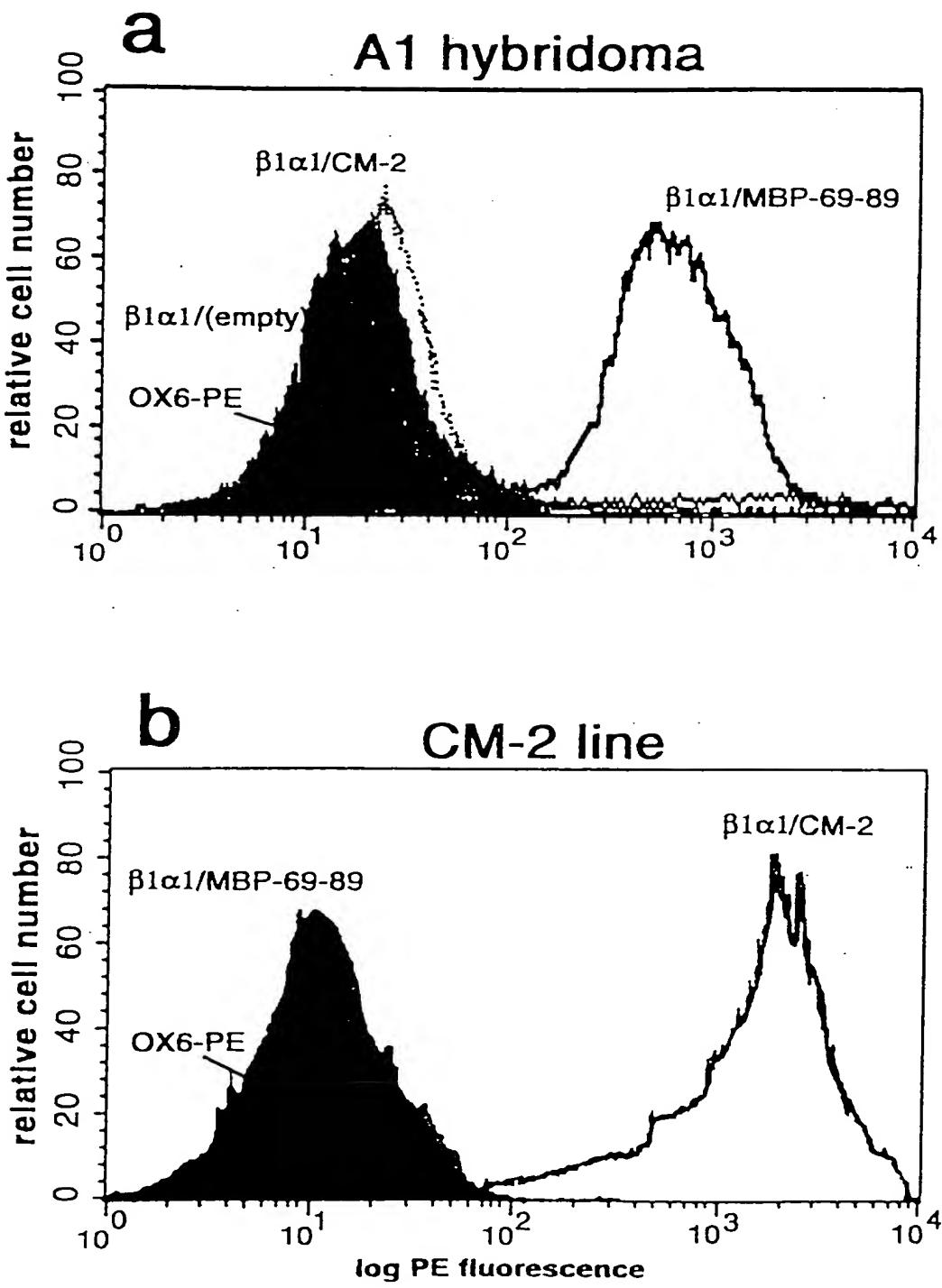


FIG. 3  
4/15

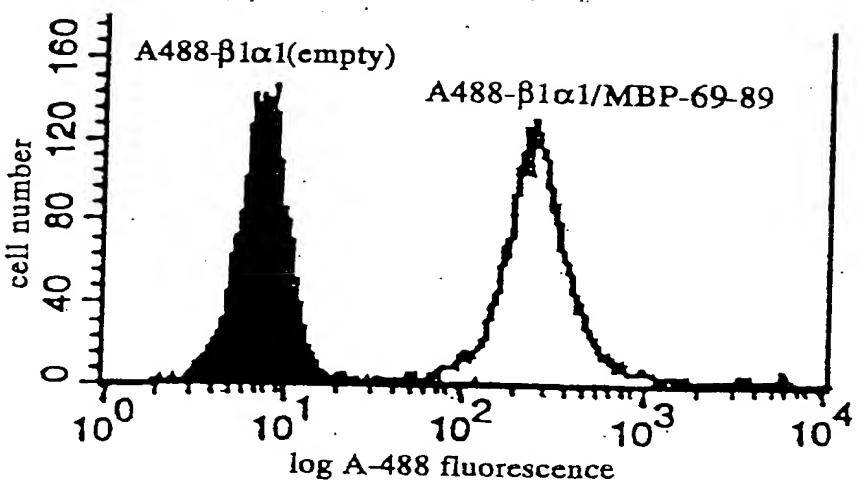


FIG. 4

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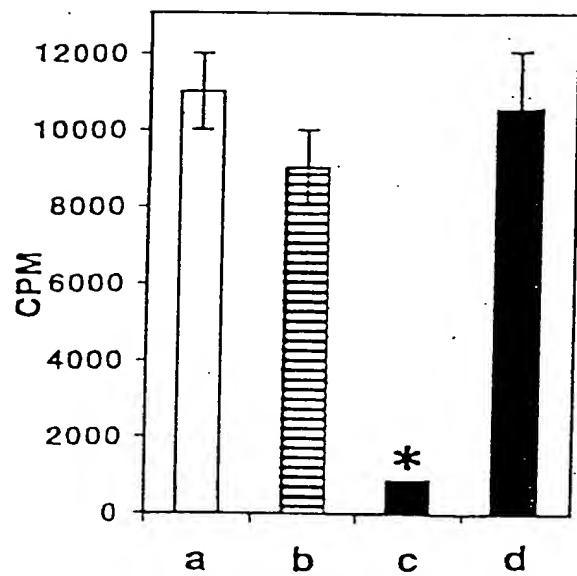


FIG. 5  
6/15

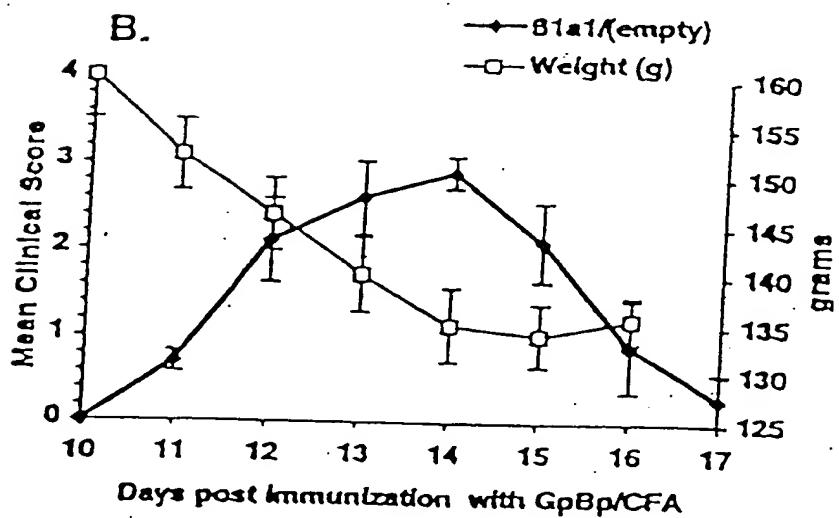
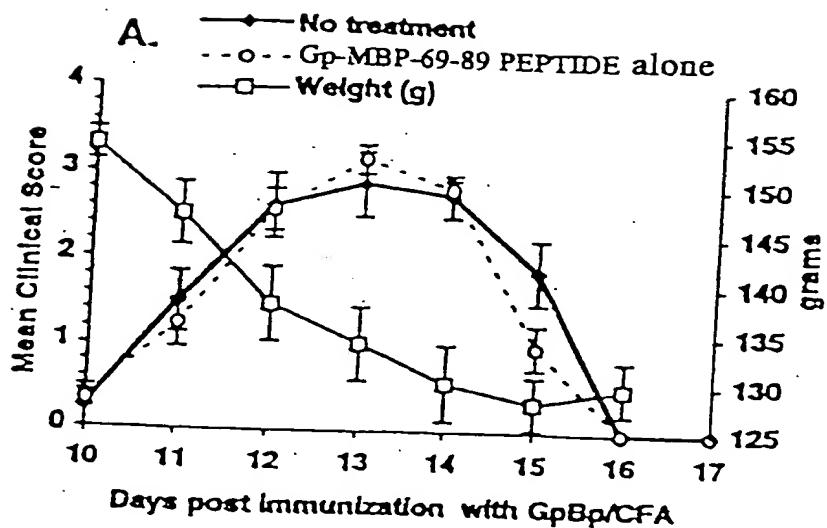


FIG. 6A  
7/15

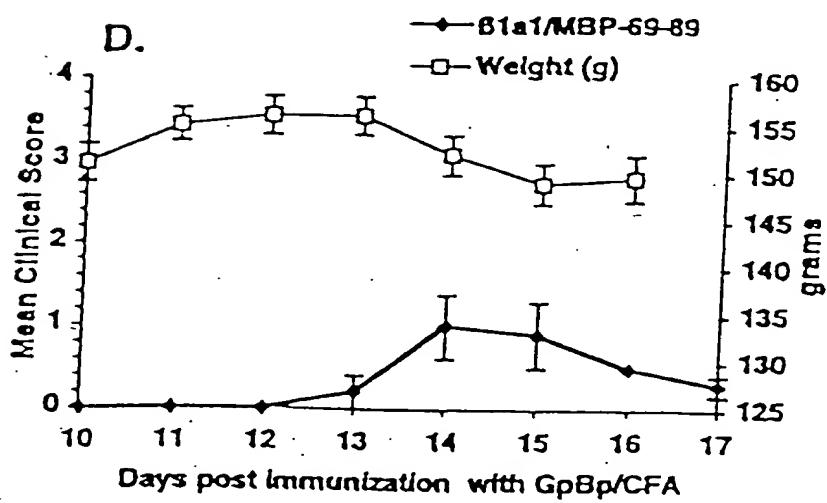
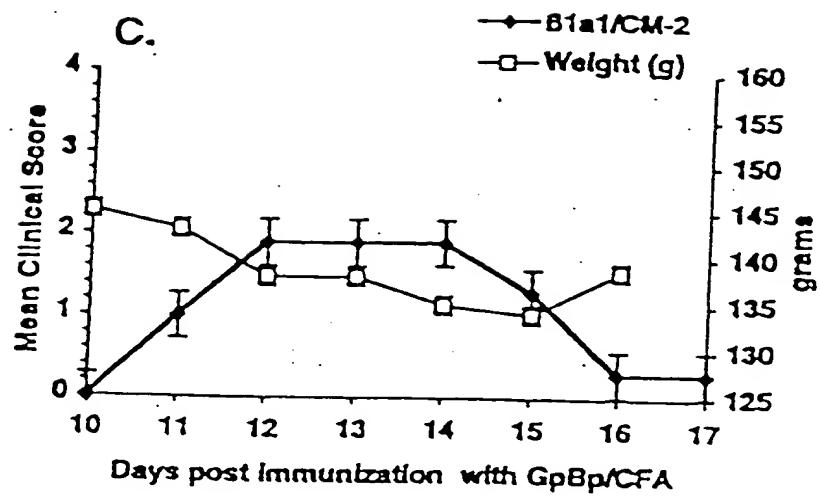


FIG. 6B  
8/15

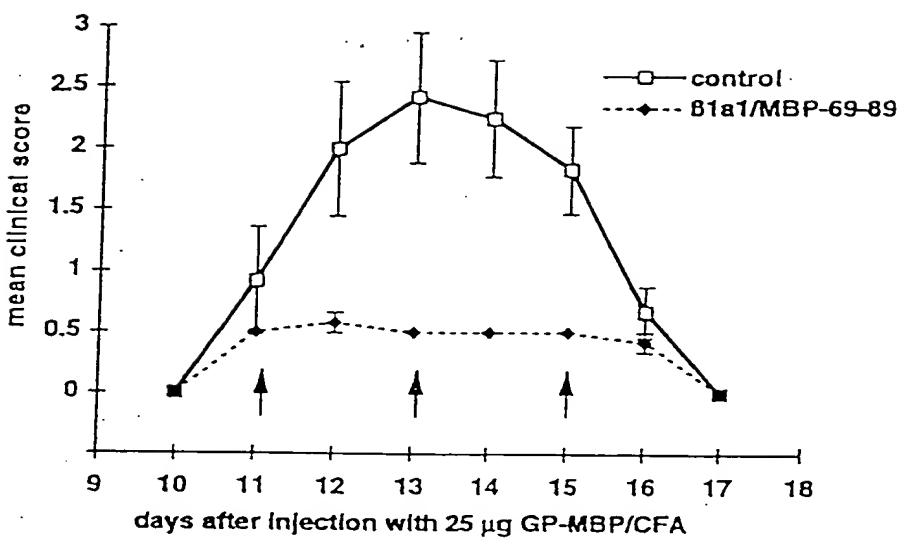


FIG. 7  
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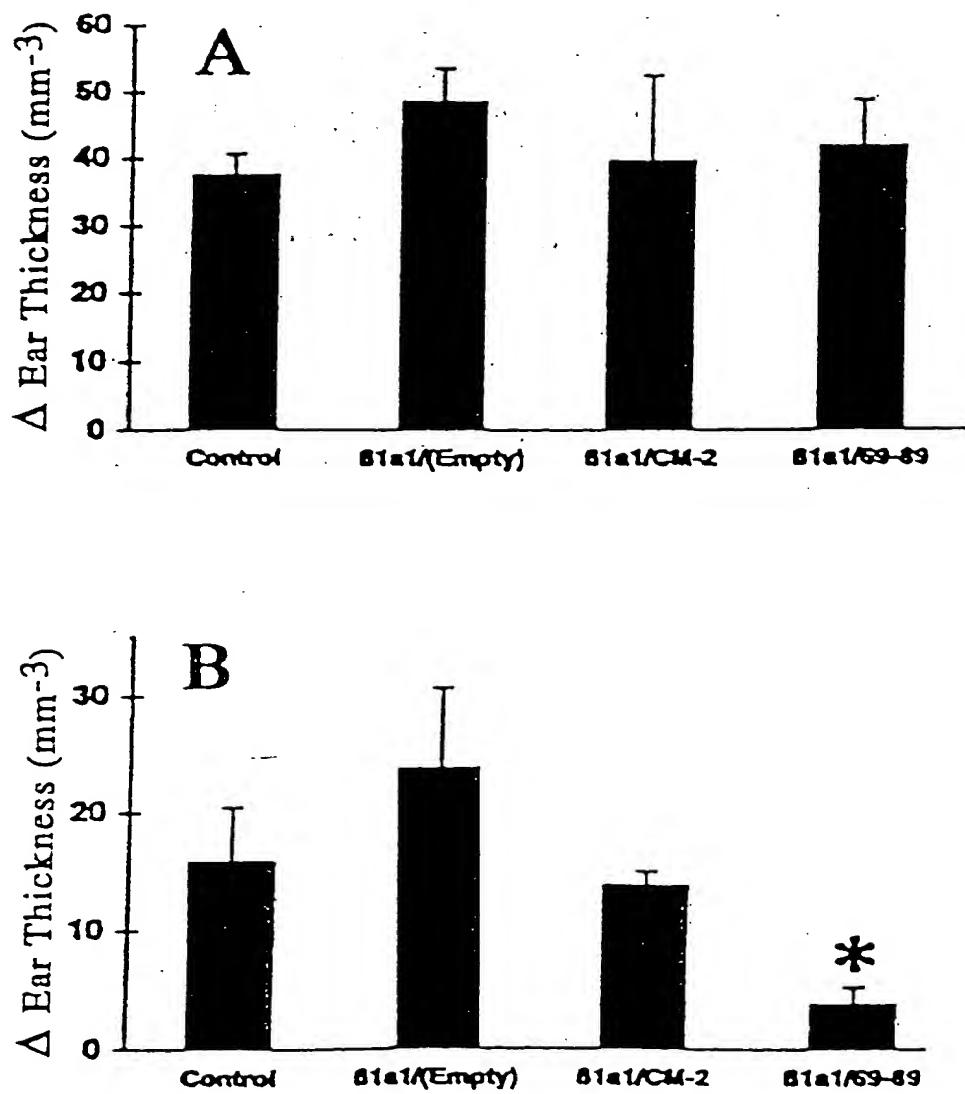


FIG. 8  
10/15

bioactive substances, growth factors, cytokines, hormones, and other regulatory molecules.

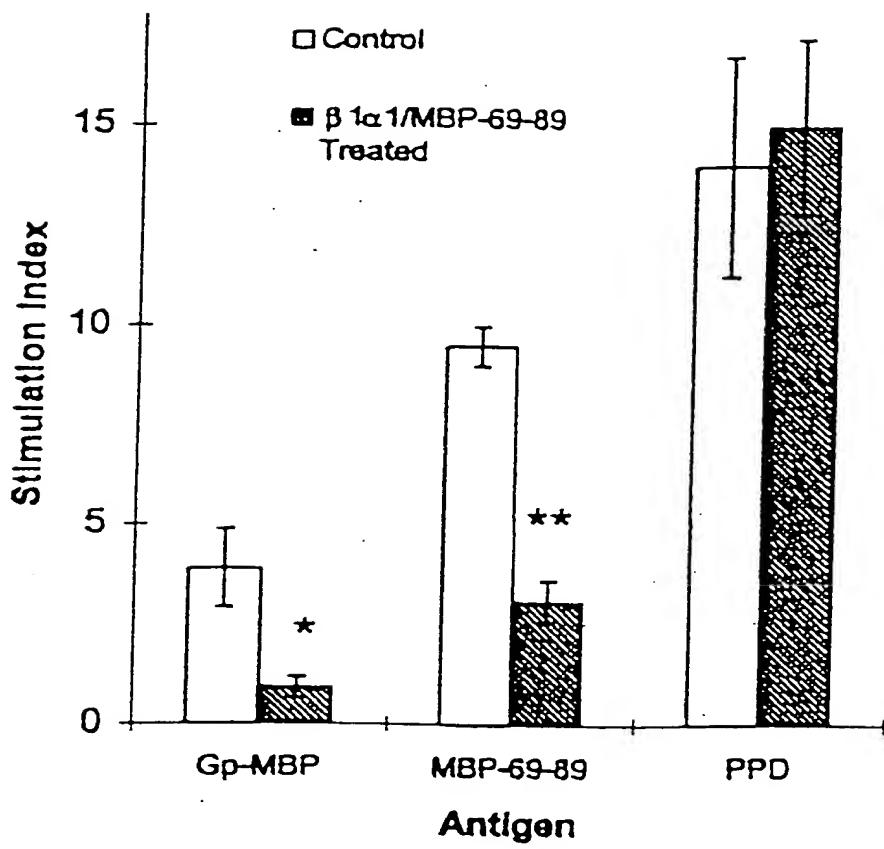


FIG. 9  
11/15

$\beta_1$  domain:

ARG4-PRO5-ARG6-PHE7-LEU8-TRP9-GLN10-LEU11-LYS12-PHE13-GLU14-CYS15-HIS16-PHE17-PHE18-ASN19-GLY20-THR21-GLU22-ARG23-VAL24-ARG25-LEU26-LEU27-GLU28-ARG29-CYS30-ILE31-TYR32-ASN33-GLN34-GLU35-GLU36-SER37-VAL38-ARG39-PHE40-ASP41-SER42-ASP43-VAL44-GLY45-GLU46-TYR47-ARG48-ALA49-VAL50-THR51-GLU52-LEU53-GLY54-ARG55-PRO56-ASP57-ALA58-GLU59-TYR60-TRP61-ASN61-ASN62-SER63-GLN64-LYS65-ASP66-LEU67-LEU68-GLU69-GLN70-ARG71-ARG72-ALA73-ALA74-VAL75-ASP76-THR77-TYR78-CYS79-ARG80-HIS81-ASN82-TYR83-GLY84-VAL85-GLY86-GLU87-SER88-PHE89-THR90-VAL91-GLN92-ARG93-ARG94-VAL95

$\alpha_1$  domain:

GLU3-GLU4-HIS5-VAL6-ILE7-ILE8-GLN9-ALA10-GLU11-PHE12-TYR13-LEU14-ASN15-PRO16-ASP17-GLN18-SER19-GLY20-GLU21-PHE22-MET23-PHE24-ASP25-PHE26-ASP27-GLY28-ASP29-GLU30-ILE31-PHE32-HIS33-VAL34-ASP35-MET36-ALA37-LYS38-LYS39-GLU40-THR41-VAL42-TRP43-ARG44-LEU45-GLU46-GLU47-PHE48-GLY49-ARG50-PHE51-ALA52-SER53-PHE54-GLU55-ALA56-GLN57-GLY58-ALA59-LEU60-ALA61-ASN62-ILE63-ALA64-VAL65-ASP66-LYS67-ALA68-ASN69-LEU70-GLU71-ILE72-MET73-THR74-LYS75-ARG76-SER77-ASN78-TYR79-THR80-PRO81-ILE82-THR83-ASN84

FIG. 10A  
12/15

$\beta_1$  domain:

ARG4-PRO5-TRP6-PHE7-LEU8-GLU9-TYR10-CYS11-LYS12-SER13-GLU14-CYS15-HIS16-PHE17-TYR18-ASN19-GLY20-THR21-GLN22-ARG23-VAL24-ARG25-LEU26-LEU27-VAL28-ARG29-TYR30-PHE31-TYR32-ASN33-LEU34-GLU35-GLU36-ASN37-ALA49-VAL50-THR51-GLU52-LEU53-GLY54-ARG55-PRO56-ASP57-ALA58-GLU59-ASN60-TRP61-ASN62-SER63-GLN64-PRO65-GLU66-PHE67-LEU68-GLU69-GLN70-LYS71-ARG72-ALA73-GLU74-VAL75-ASP76-THR77-VAL78-CYS79-ARG80-HIS81-ASN82-TYR83-GLU84-ILE85-PHE86-ASP87-ASN88-PHE89-LEU90-VAL91-PRO92-ARG93-ARG94-VAL95

$\alpha_1$  domain:

GLU3-GLU4-HIS5-THR6-ILE7-ILE8-GLN9-ALA10-GLU11-PHE12-TYR13-LEU14-PHE15-PRO16-ASP17-LYS18-ARG19-GLY20-GLU21-PHE22-MET23-PHE24-ASP25-PHE26-ASP27-GLY28-ASP29-GLU30-ILE31-PHE32-HIS33-VAL34-ASP35-ILE36-GLU37-LYS38-SER39-GLU40-THR41-ILE42-TRP43-ARG44-LEU45-GLU46-GLU47-PHE48-ALA49-LYS50-PHE51-ALA52-SER53-PHE54-GLU55-ALA56-GLN57-GLY58-ALA59-LEU60-ALA61-ASN62-ILE63-ALA64-VAL65-ASP66-LYS67-ALA68-ASN69-LEU70-ASP71-VAL72-MET73-LYS74-GLU75-ARG76-SER77-ASN78-ASN79-THR80-PRO81-ASP82-ALA83-ASN84

$\beta_1$  domain:

NET (-2)-GLY (-1)-ARG1-ASP2-SER3-PRO4-ARG5-ASP6-PHE7-VAL8-TYR9-  
GLN10-PHE11-LYS12-GLY13-LEU14-CYS15-TYR16-TYR17-THR18-ASN19-GLY20-  
THR21-GLN22-ARG23-ILE24-ARG25-ASP26-VAL27-ILE28-ARG29-TYR30-ILE31-  
TYR32-ASN33-GLN34-GLU35-GLU36-TYR37-LEU38-ARG39-TYR40-ASP41-SER42-  
ASP43-VAL44-GLY45-GLU46-TYR47-ARG48-ALA49-LEU50-THR51-GLU52-LEU53-  
GLY54-ARG55-PRO56-SER57-ALA58-GLU59-TYR60-TRP61-ASN62-SER63-GLN64-  
LYS65-GLN66-TYR67-LEU68-GLU69-GLN70-THR71-ARG72-ALA73-GLU74-LEU75-  
ASP76-THR77-VAL78-CYS79-ARG80-HIS81-ASN82-TYR83-GLU84-GLY85-SER86-  
GLU87-VAL88-ARG89-THR90-SER91-LEU92-ARG93-ARG94-LEU95

$\alpha_1$  domain:

ALA2-ASP3-HIS4-VAL5-ALA6-ALA7-TYR8-GLY9-ILE10-ASN11-MET12-TYR13-  
GLN14-TYR15-TYR16-GLU17-SER18-ARG19-GLY20-GLN21-PHE22-THR23-HIS24-  
GLU25-PHE26-ASP27-GLY28-ASP29-GLU30-GLU31-PHE32-TYR33-VAL34-ASP35-  
LEU36-ASP37-LYS38-LYS39-GLU40-THR41-ILE42-TRP43-ARG44-ILE45-PRO46-  
GLU47-PHE48-GLY49-GLN50-LEU51-THR52-SER53-PHE54-ASP55-PRO56-GLN57-  
GLY58-GLY59-LEU60-GLN61-ASN62-ILE63-ALA64-ILE65-ILE66-LYS67-HIS68-  
ASN69-LEU70-GLU71-ILE72-LEU73-MET74-LYS75-ARG76-SER77-ASN78-SER79-  
THR80-GLN81-ALA82-VAL83-ASN84

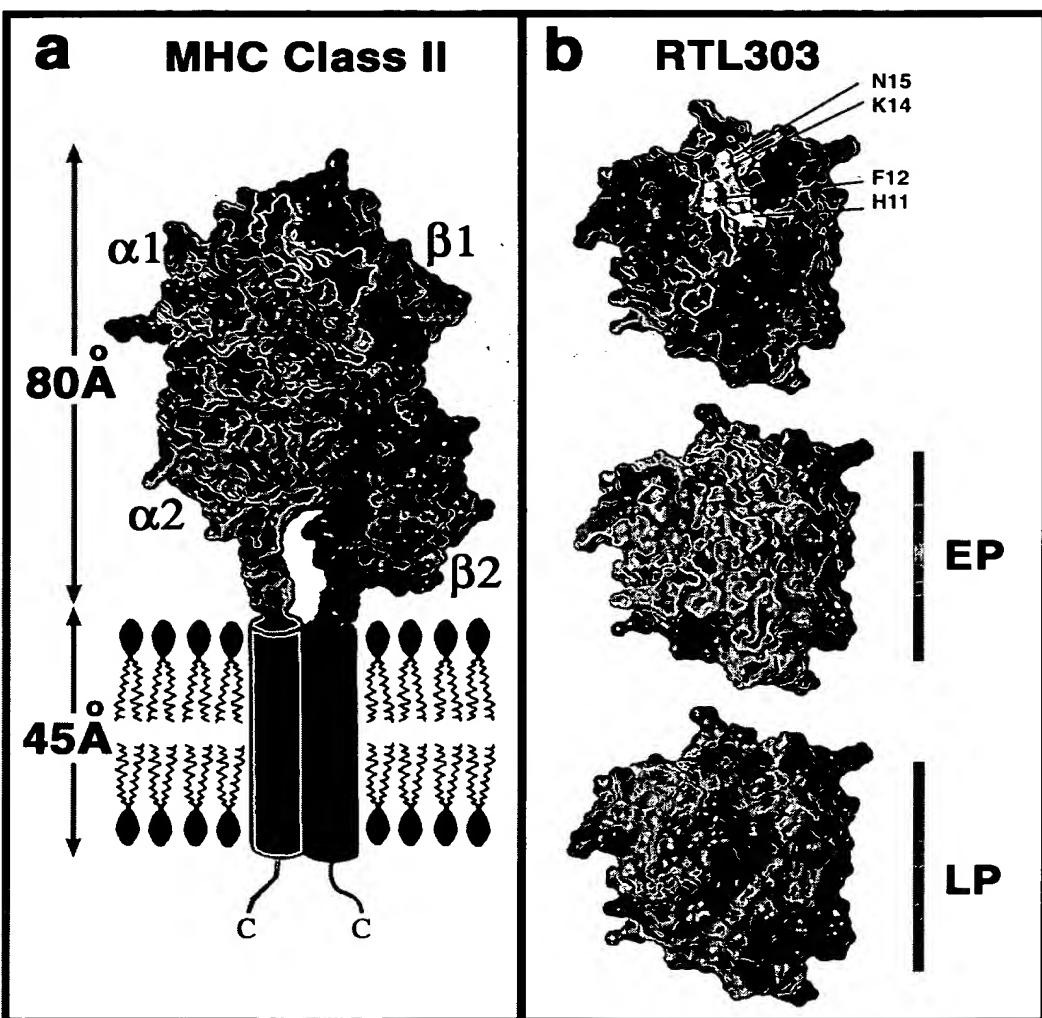
$\alpha_1$  domain:

GLY1-SER2-HIS3-SER4-MET5-ARG6-TYR7-PHE8-TYR9-THR10-ALA11-MET12-SER13-ARG14-PRO15-GLY16-ARG17-GLY18-GLU19-PRO20-ARG21-PHE22-ILE23-ALA24-VAL25-GLY26-TYR27-VAL28-ASP29-ASP30-THR31-GLN32-PHE33-VAL34-ARG35-PHE36-ASP37-SER38-ASP39-ALA40-ALA41-SER42-PRO43-ARG44-THR45-GLU46-PRO47-ARG48-PRO49-PRO50-TRP51-ILE52-GLU53-GLN54-GLU55-GLY56-PRO57-GLU58-TYR59-TRP60-ASP61-ARG62-ASN63-THR64-GLN65-ILE66-PHE67-LYS68-THR69-ASN70-THR71-GLN72-THR73-TYR74-ARG75-GLU76-ASN77-LEU78-ARG79-ILE80-ALA81-LEU82-ARG83-TYR84-

$\alpha_2$  domain:

TYR85-ASN86-GLN87-SER88-GLU89-ALA90-GLY91-SER92-HIS93-ILE94-ILE95-GLN96-ARG97-MET98-TYR99-GLY100-CYS101-ASP102-LEU103-GLY104-PRO105-ASP106-GLY107-ARG108-LEU109-LEU110-ARG111-GLY112-HIS113-ASP114-GLN115-SER116-ALA117-TYR118-ASP119-GLY120-LYS121-ASP122-TYR123-ILE124-ALA125-LEU126-ASN127-GLU128-ASP129-LEU130-SER131-SER132-TRP133-THR134-ALA135-ALA136-ASP137-THR138-ALA139-ALA140-GLN141-ILE142-THR143-GLN144-ARG145-LYS146-TRP147-GLU148-ALA149-ALA150-ARG151-VAL152-ALA153-GLU154-GLN155-LEU156-ARG157-ALA158-TYR159-LEU160-GLU161-GLY162-LEU163-CYS164-VAL165-GLU166-TRP167-LEU168-ARG169-ARG170-TYR171-LEU172-GLU173-ASN174-GLY175-LYS176-GLU177-THR178-LEU179-GLN180-ARG181-ALA182-ASP183-PRO184

FIG. 12



**SpeI**  
 -2 CCCATGGGACACCCGAGAAACCCGGTTGGTCACTTCTTCACATCGTTACCCCGCTGGAGGTGGCTCACTAGTGCCTGGAGGC  
 M G D T R E N P V V H F F K N I V T P R G G G S L V P R G  
 10 S G G G P R F L W Q P K R E C H F F N G T E R V R F L D R  
 ---linker---| 40 ---linker---| 50 ---linker---| 60 ---linker---| 70 ---linker---| 80 ---linker---| 90 ---linker---| 100 ---linker---| 110 ---linker---| 120 ---linker---| 130 ---linker---| 140 ---linker---| 150 ---linker---| 160 ---linker---| 170 ---linker---| 180 ---linker---| 190 ---linker---| 200 ---linker---| 210

**TCTGGAGGTGGAGGCCACGTTTCGCTGGCAGCCTAAGAGGGAGTGTCAATTCTTCATGGGACCGAGGGCTGGTCTGGACAGACA**  
**TACTCTATAACCGAGGACTCCGTGCGCTTCGACAGCAGCGACGTGGGGAGTTCCGGGGTGAACGGAGCTGGGGGGCTGACGTGAG**  
**TACTGGAAACAGCCAGAAGGACATCTGGAGCAGGGCAGACACCTACTGCGAGACACAACACTACGGGGTGTGGAGAGCTTC**  
**ACAGTGCAGGGGAGTCATCAAAGAACATGTGGATCATCCAGGCCGAGTTCTATCTGAATCCTGACCAATCAGGGAGTTATGCTT**  
**T V Q R R V I K E E H V I I Q A E F Y L N P D Q S G E F M F**  
**271 Y W N S Q K D I L E Q A R A A V D T Y C R H N Y G V V E S F**  
**361 100 110 120 130 140 150 160 170 180 190 200**

**GACTTGTATGGTGTGAGATTTCATGTGGATATGGCAAAGAAGGAGACGGCTGCTGGGGCTTGAAGAATTGGACGATTGCCAGCTT**  
**D F D G D E I F H V D M A K K E T V W R L E E F G R F A S F**  
**451 160 170 180 190 200**

**GAGGCTCAAGGTGCAATTGGCAACATAGCTGTGGACAAAGCCAACTTGAAATCATGACAAAGGGCTCCAACATATACTCCGATCACCAAT**  
**E A Q G A L A N I A V D K A N L E I M T K R S N Y T P I T N**  
**541 210**

**XbaI**  
 TAACCTCGAG  
**end**

FIG. 13

FIG. 14

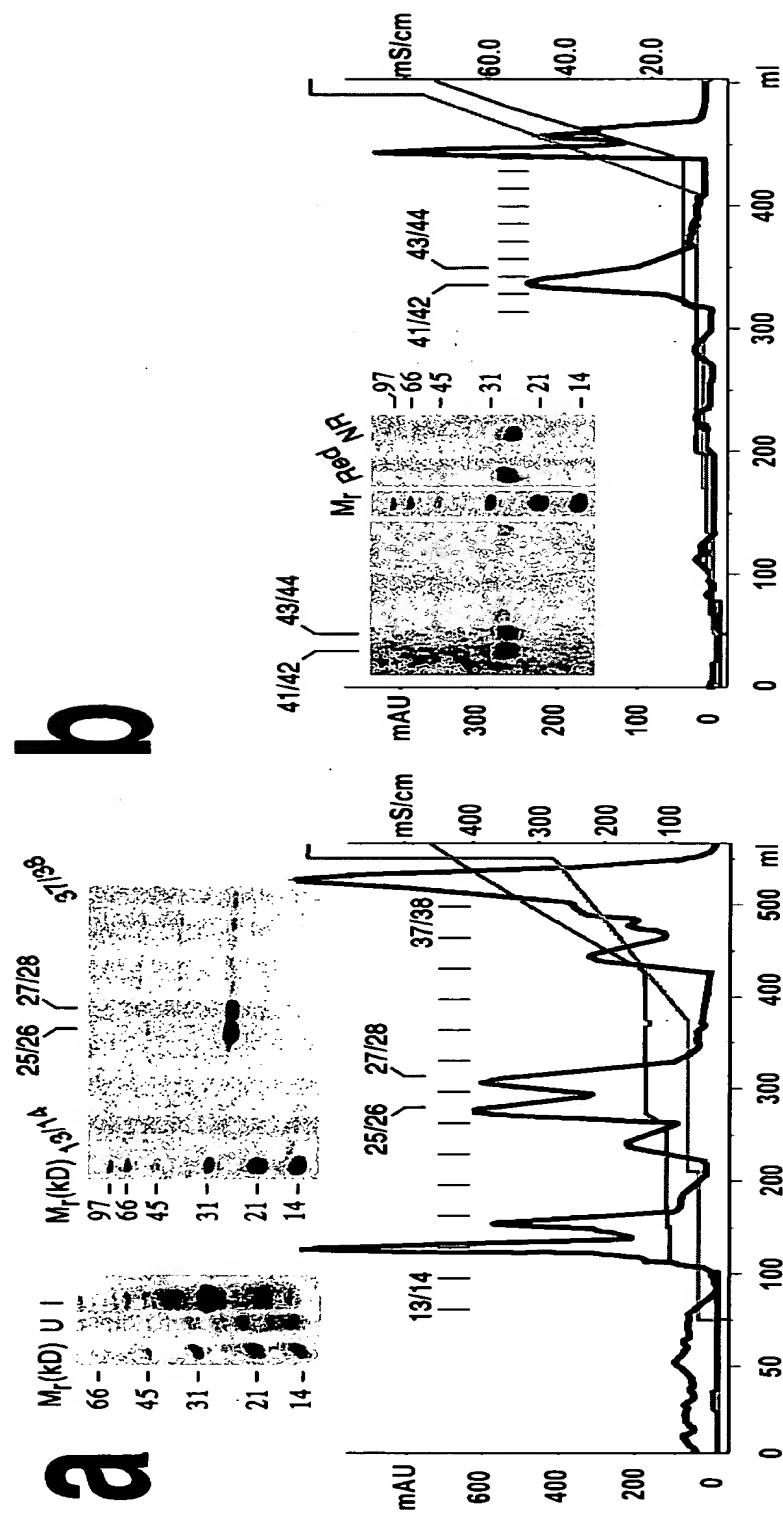


FIG. 14

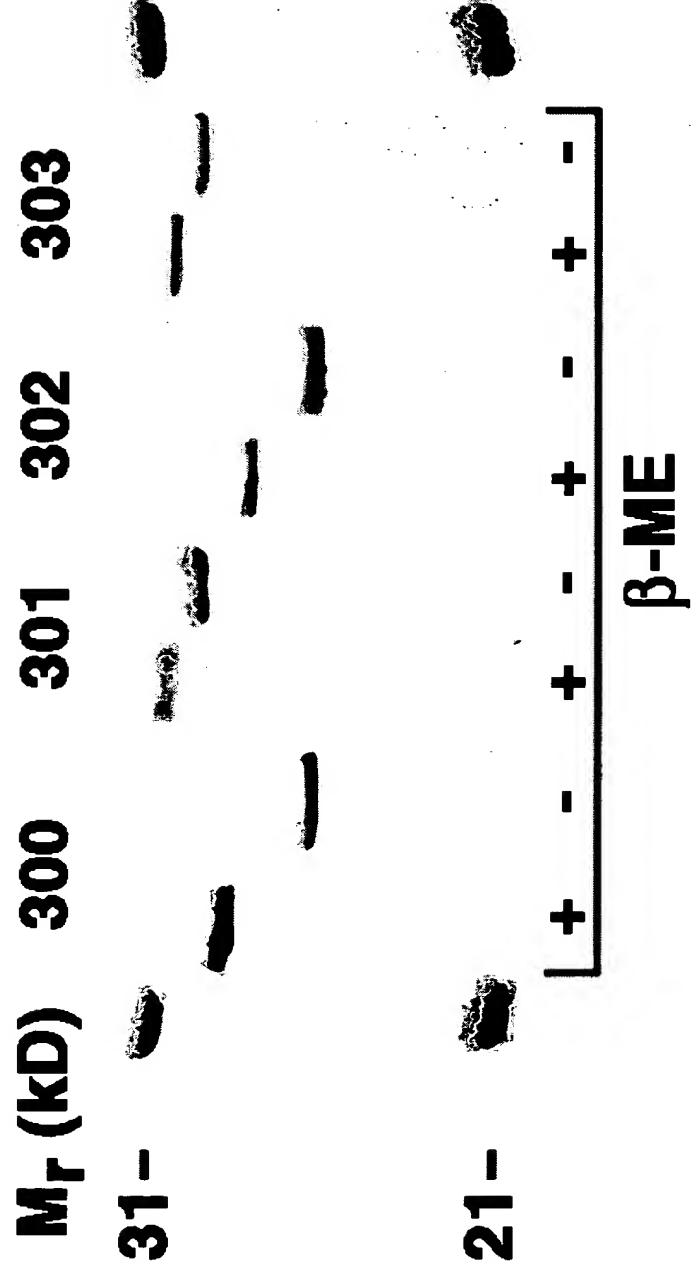


FIG. 15

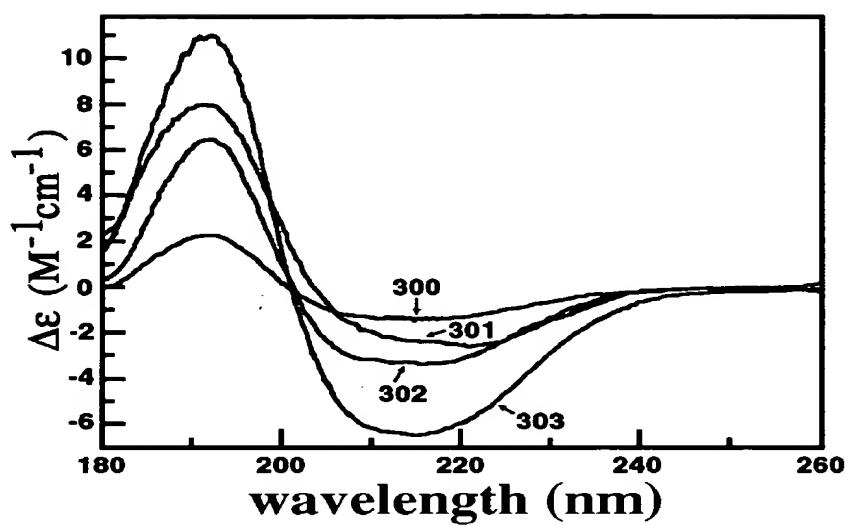


FIG. 16

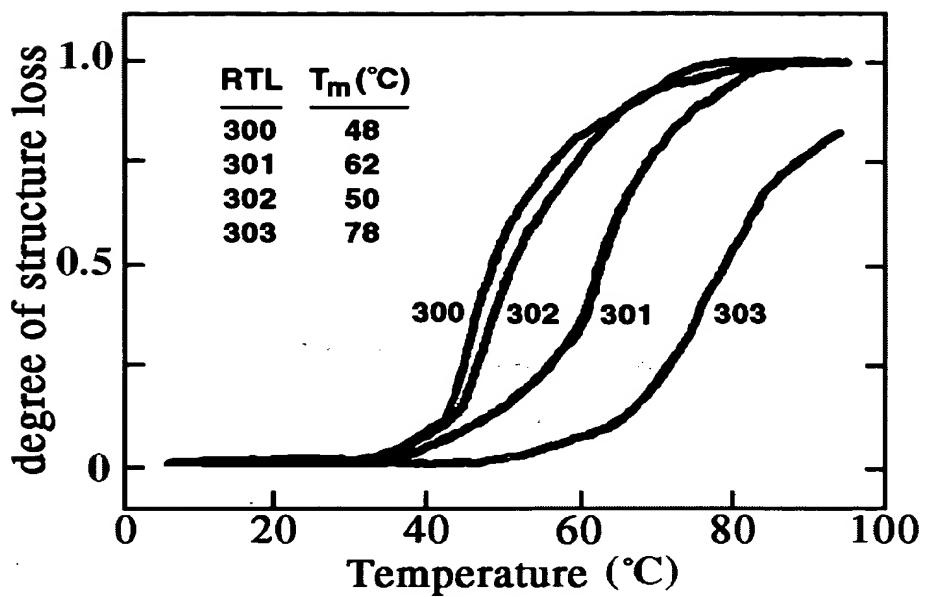
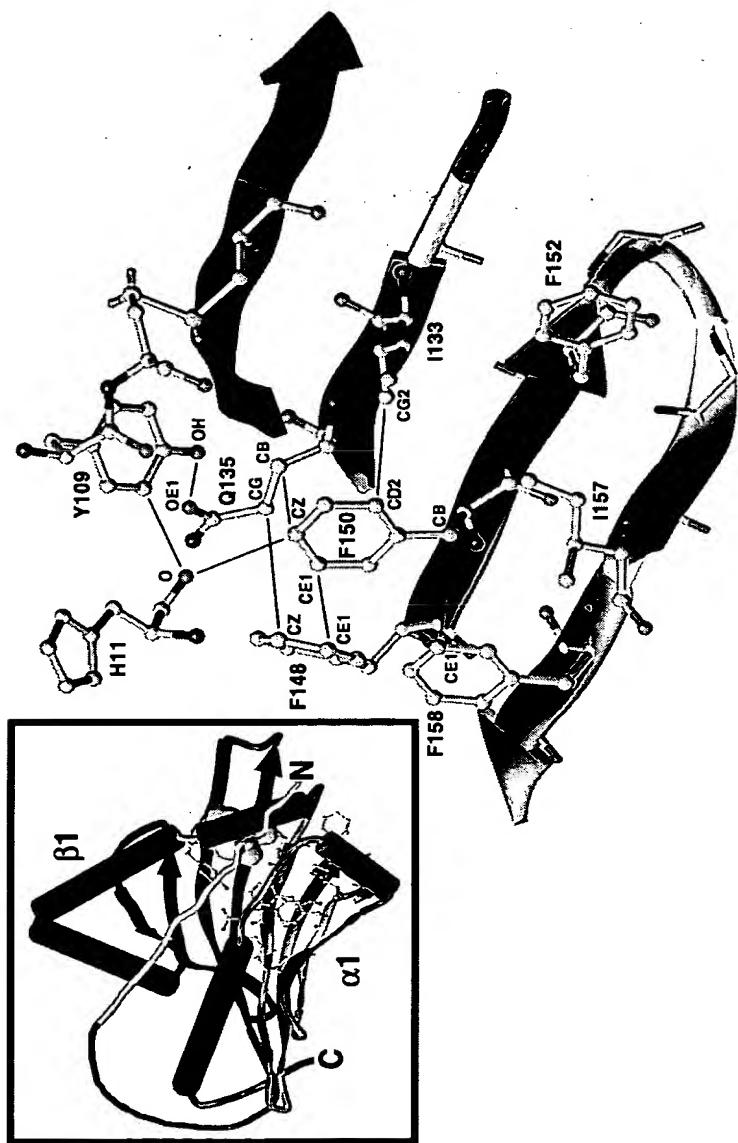


FIG. 17

FIG. 18



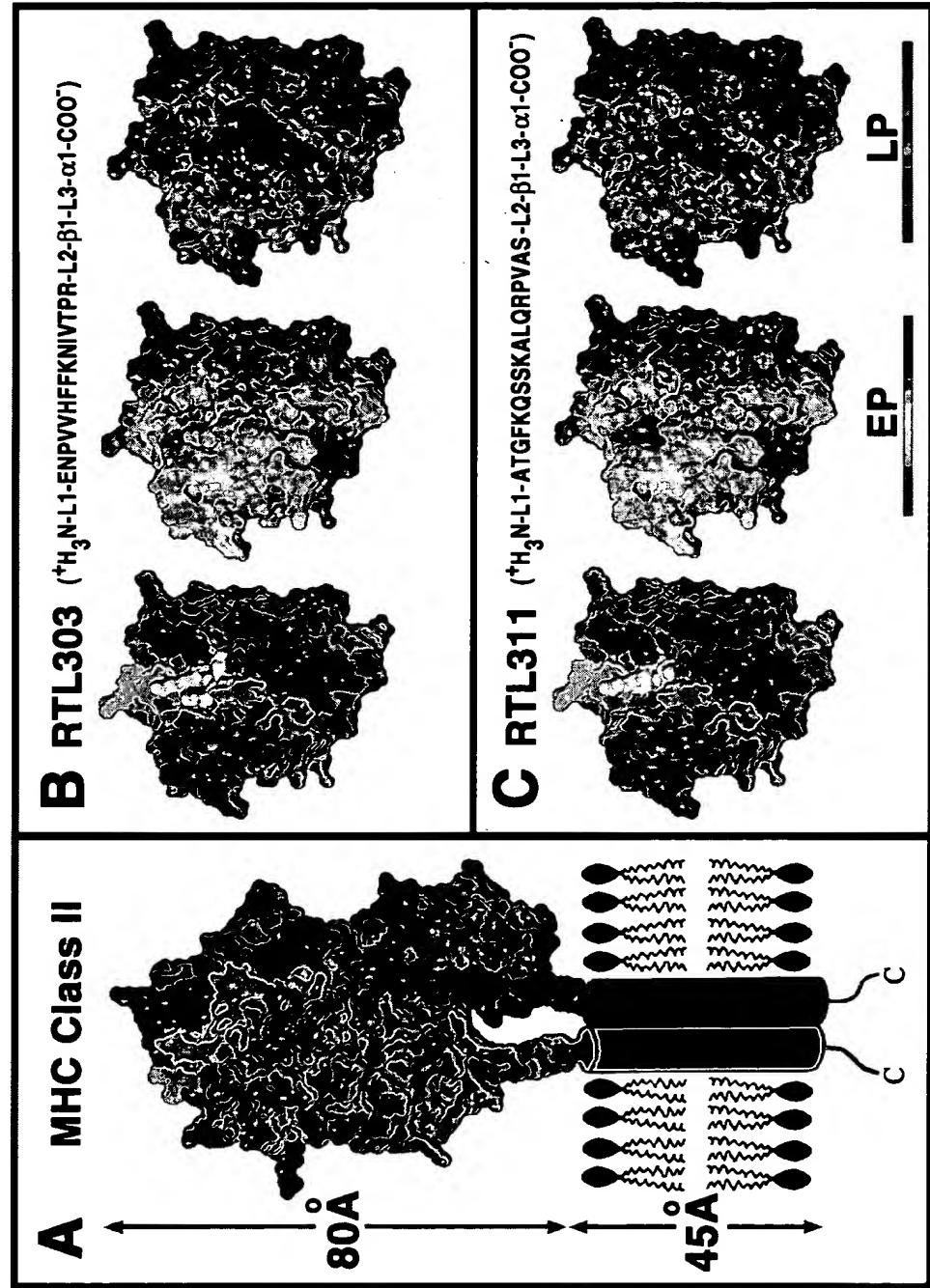
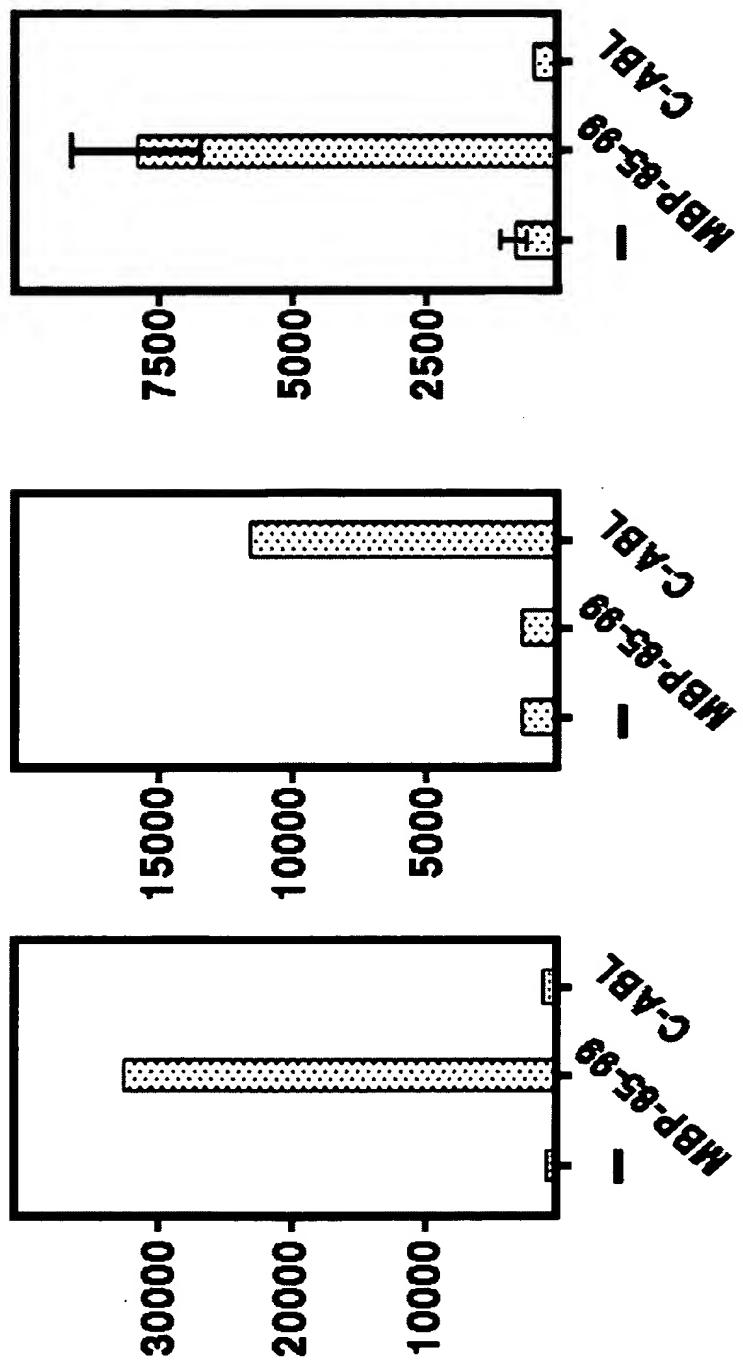


FIG. 19

**MR#3-1 MR#2-87 CP#1-15**



**CPM**

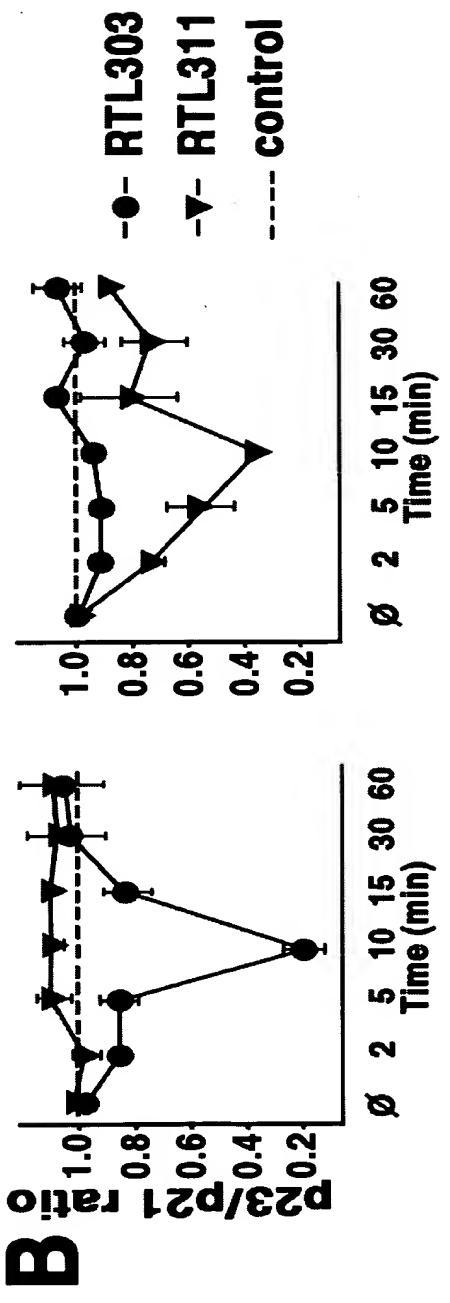
**FIG. 20**

FIG. 21 A

#3-1      #2-87



FIG. 21 B



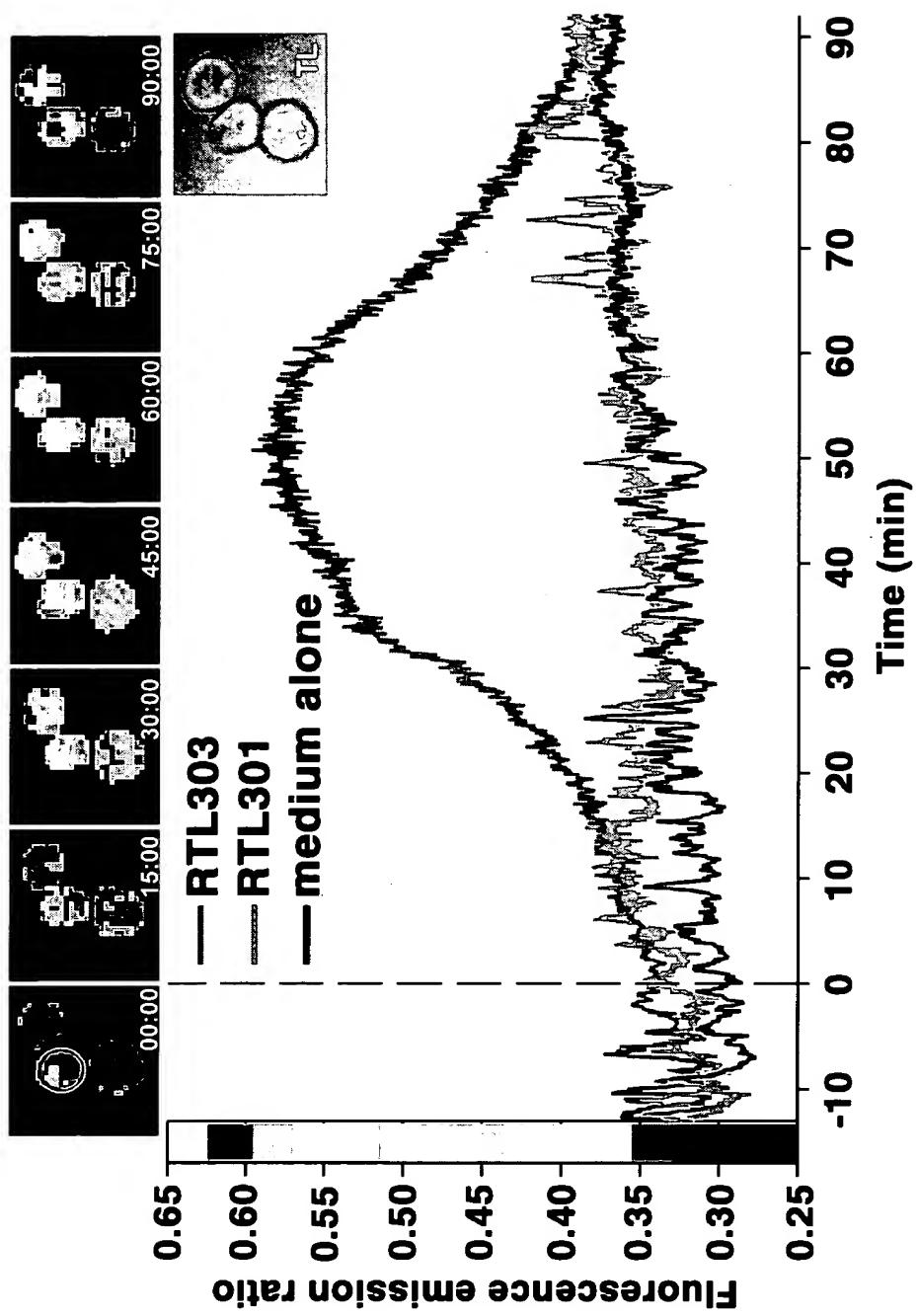
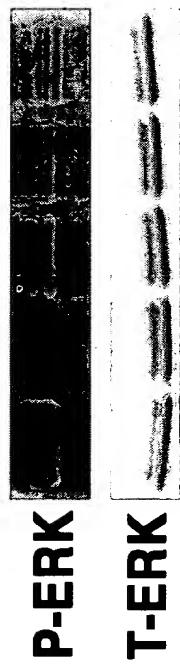


FIG. 22

FIG. 23 A

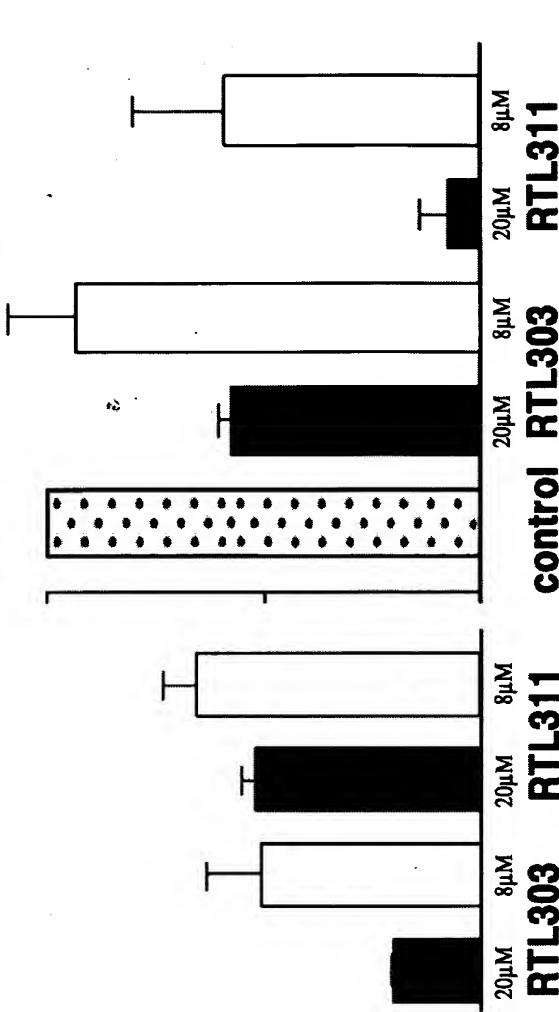
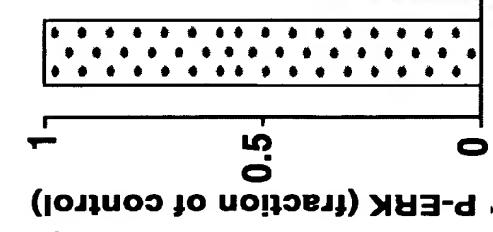
#3-1



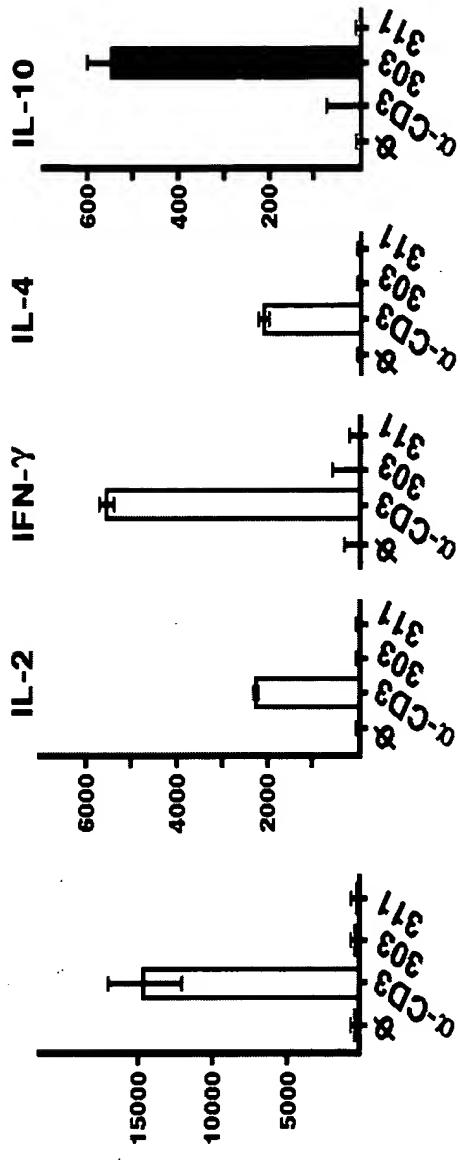
#2-87



FIG. 23 B



**FIG. 24 A MMR#3-1**



**FIG. 24 B MMR#2-87**

